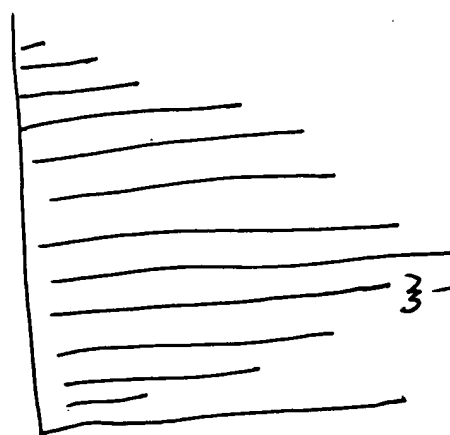


↓ RE Digest / Separate by length STEP 1



3 — subset of interest

STEP 2

### STEP 3

↓ purification

STEP 4

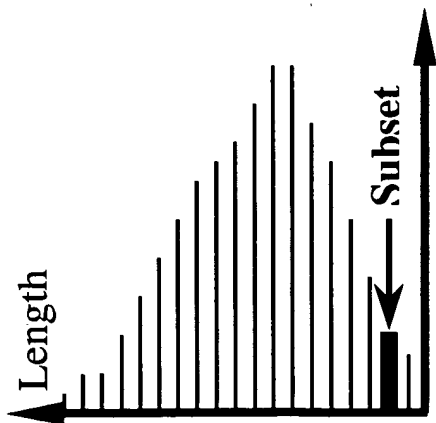
## Isolated fragments STEPS

Figure 2

FIGURE 2

Total Genome  
 $3.3 \times 10^9$  bp

RE Digestion



Size Selection

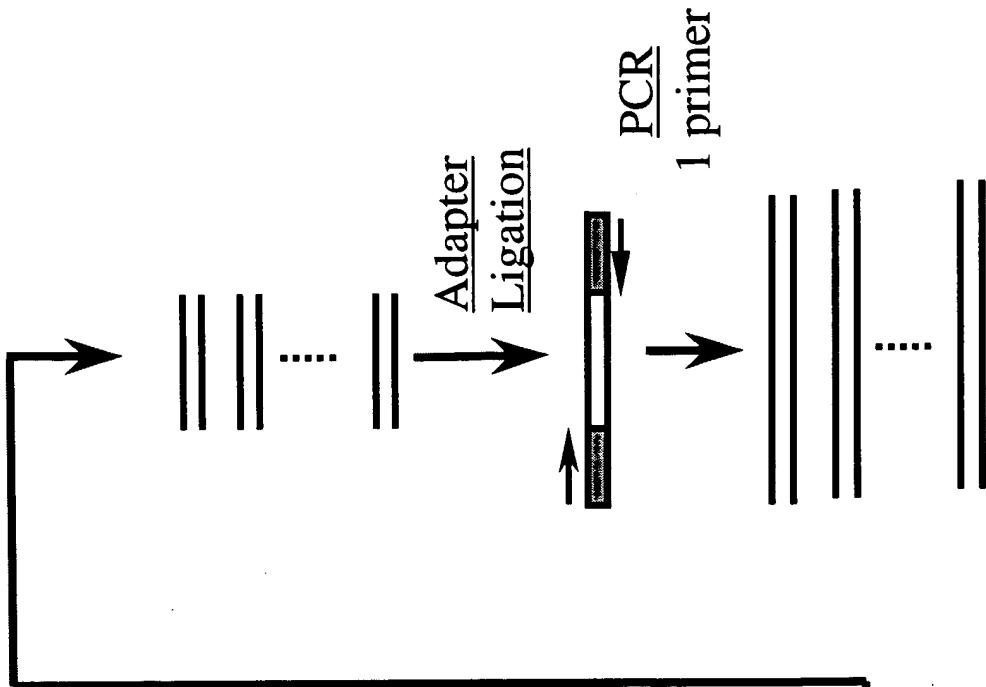


Figure 3

# Effects of Complexity

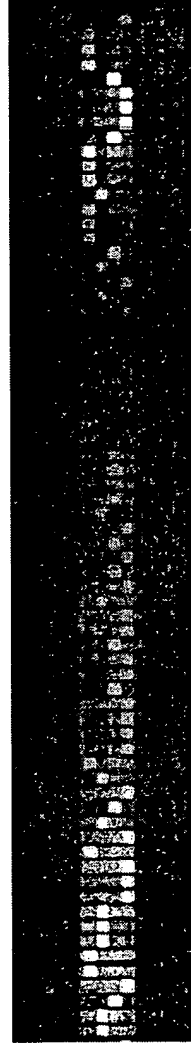
(A, C, G, T)-HGE250-350; ~16Mb



PCR Primer



(A, T)-HGE250-350; ~4Mb



(T)-HGE250-350; ~1Mb

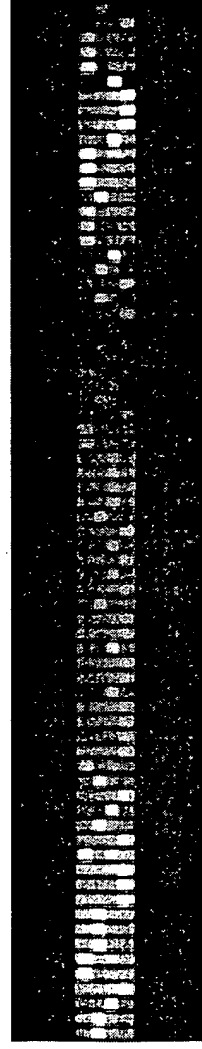


FIGURE 4

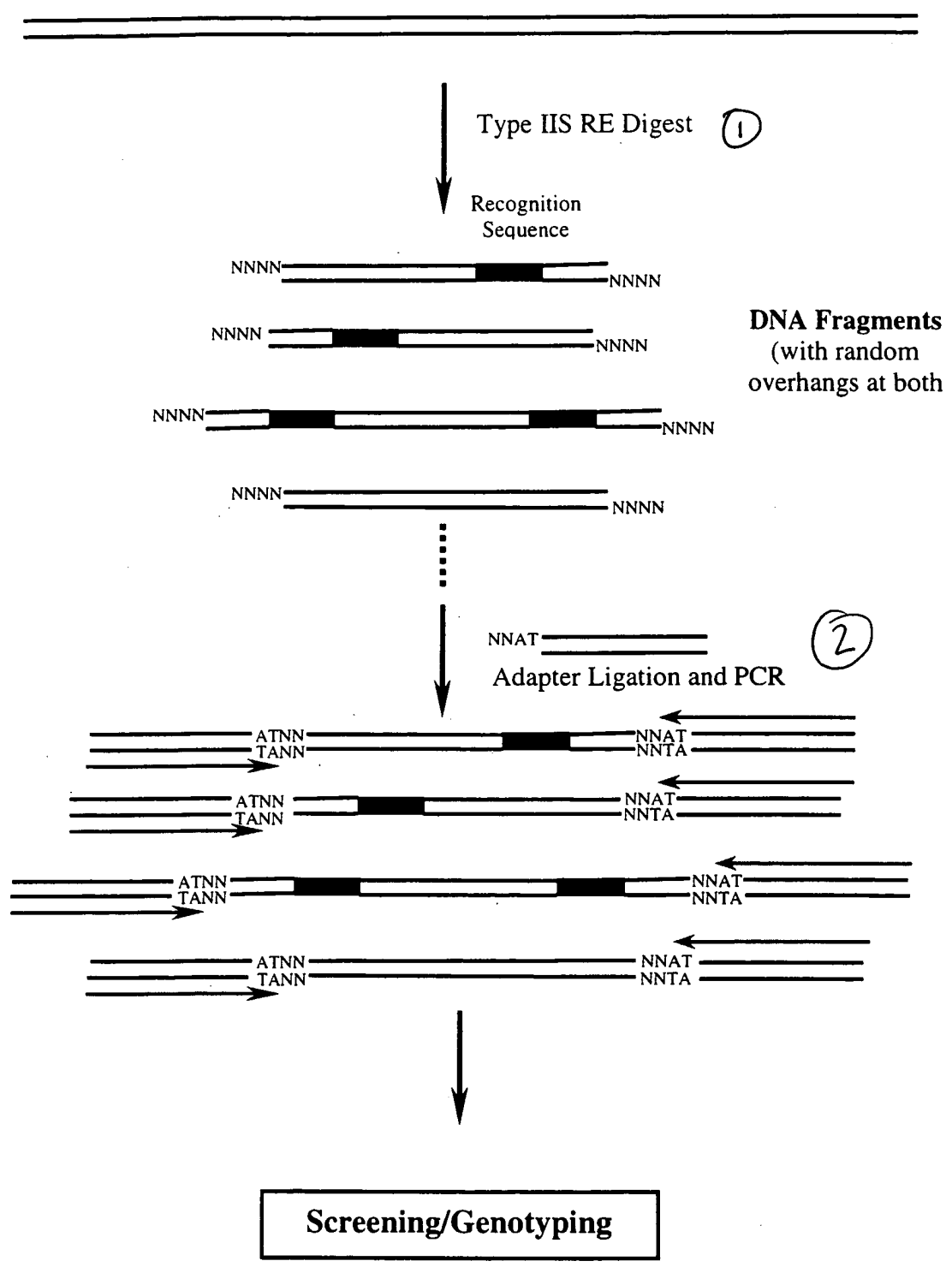


FIGURE 5



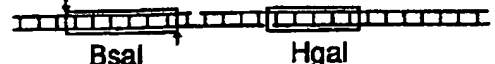
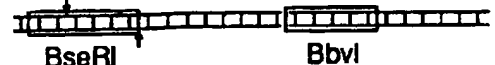
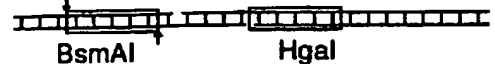




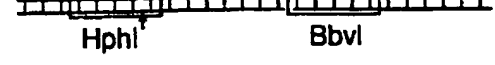

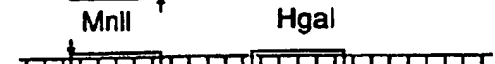



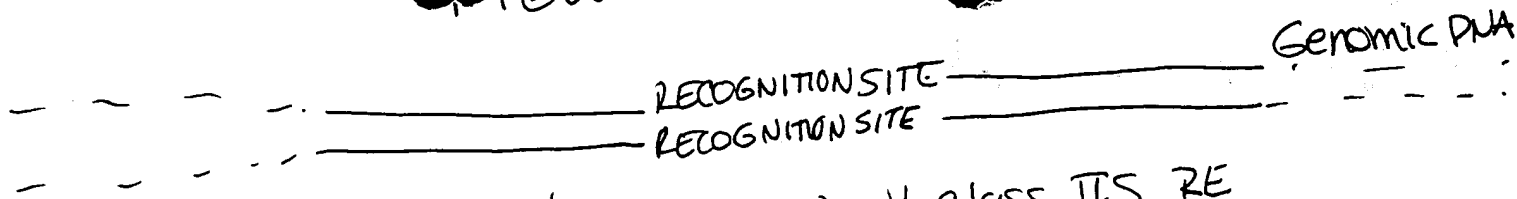
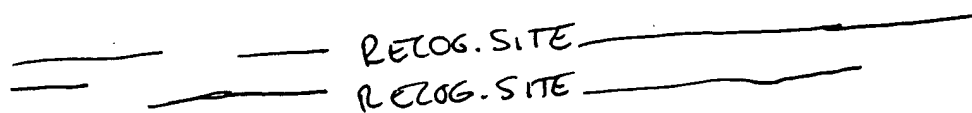
	cleavage Frequency of first enzyme	sites in $\lambda$	size of captured sequence (bp)
	1/512	58	5
	1/2048	24	6
	1/2048	2	5
	1/2048	19	8
	1/512	37	5
	1/2048	41	8
	1/2048	14	5
	1/2048	34	4
	1/512	102	10
	1/512	168	7
	1/512	130	7
	1/128	262	6
	1/512	61	5
	1/8192	10	4
	1/512	169	9

Fig. 1

# FIGURE 6



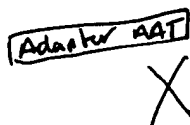
↓ DIGESTION w/ class II RE



↓ ligation



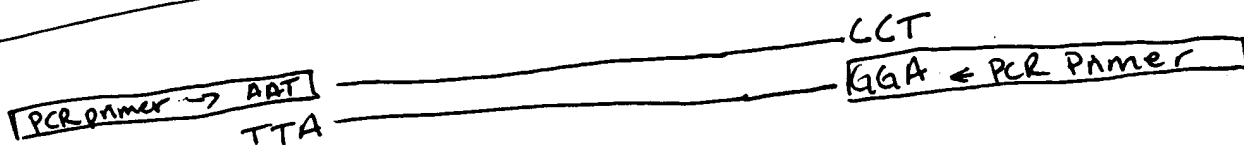
ligation



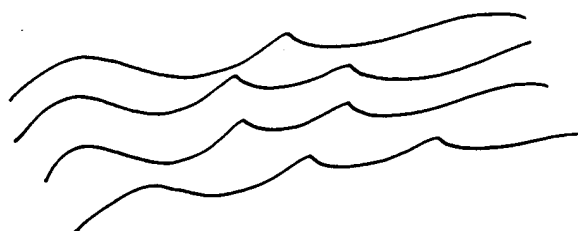
CTT

no ligation

A.



↓ amplification

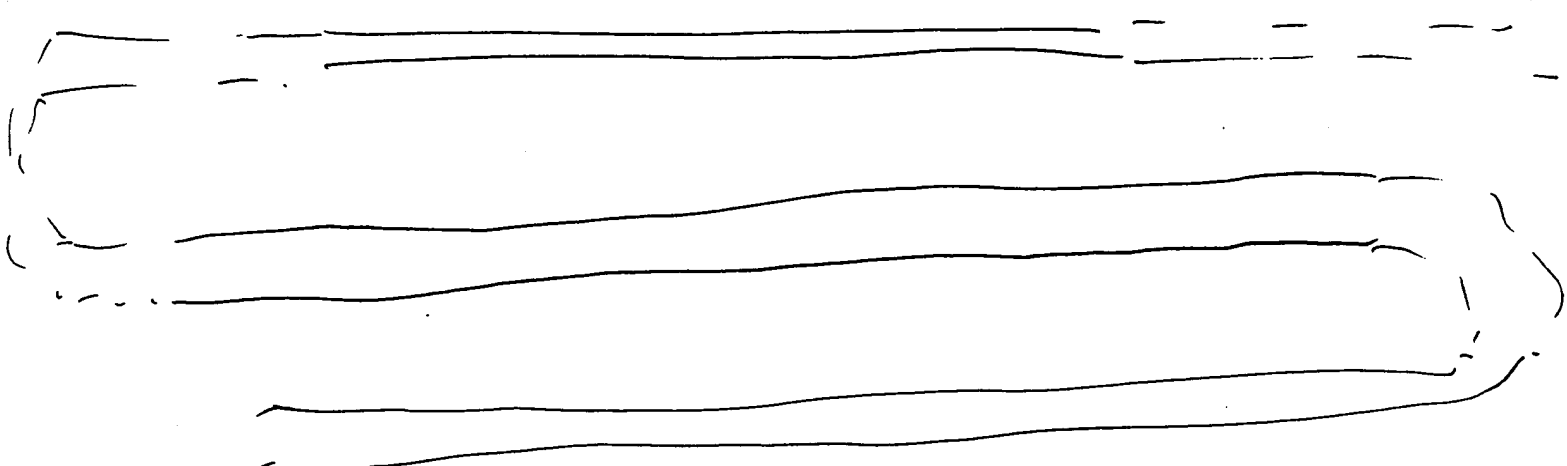


CCT = AAG not amplified

B.

# Figure 7

total genomic DNA



\*nncgttgg→

←nnnnngc



total genomic DNA

## Complexity of AP Amplified Human Genomic DNA

Primer	Sequence	Annealing T	Polymerase	# Present	/
Total Genome				434	6.1
sdp5	nncgttgg	30	ThermoSequenase	393	5.6
sdp3	agagctgc	30	TaqGold	264	3.7
DOP	ccgactcgagnnnnnnatgtgg	30	TaqGold	247	3.5
sdp8	nnnnnnngccgttgg	45	TaqGold	218*	3.1*
sdp8-10	nnnnnatgccgttgg	45	TapGold	206	2.9
sdp8	nnnnnnngccgttgg	55	TaqGold	114	1.6

\* Results of 20 µg/200µl hybridization.



## Reproducibility of AP PCR

Independent preps of sdp8/H.G. DNA(B.M.)/45°C

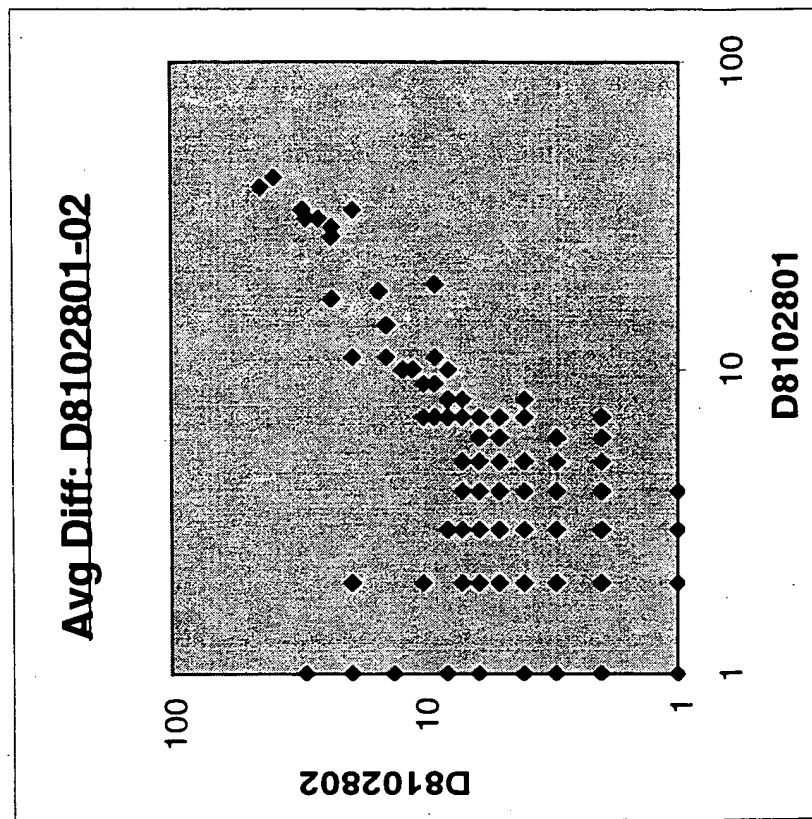
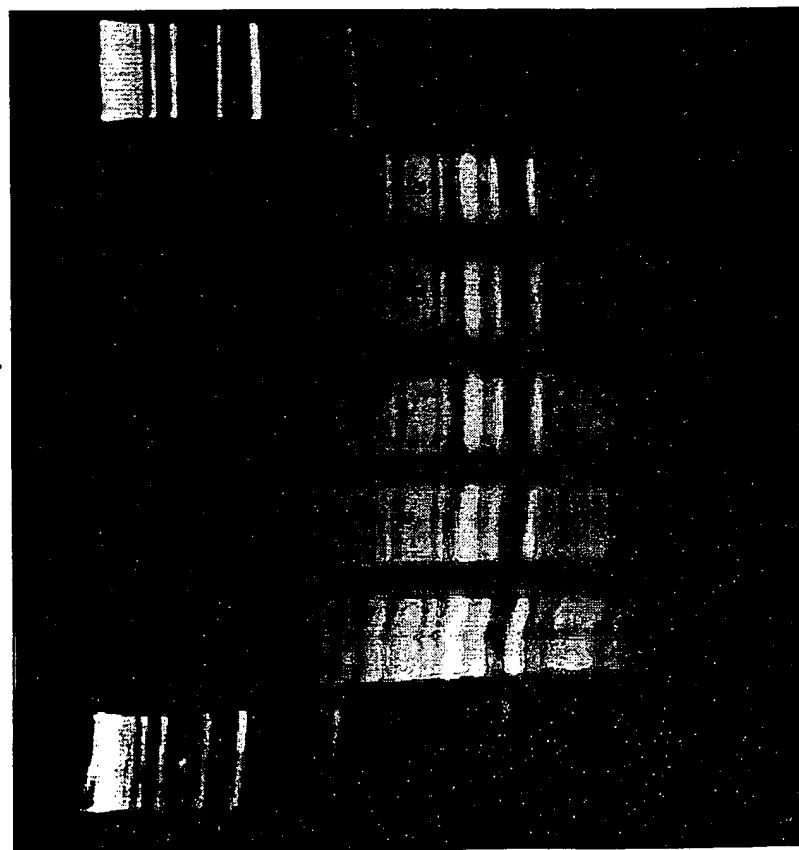


FIGURE 10

## A Novel Way of Removing repetitive sequences from Genomic DNA

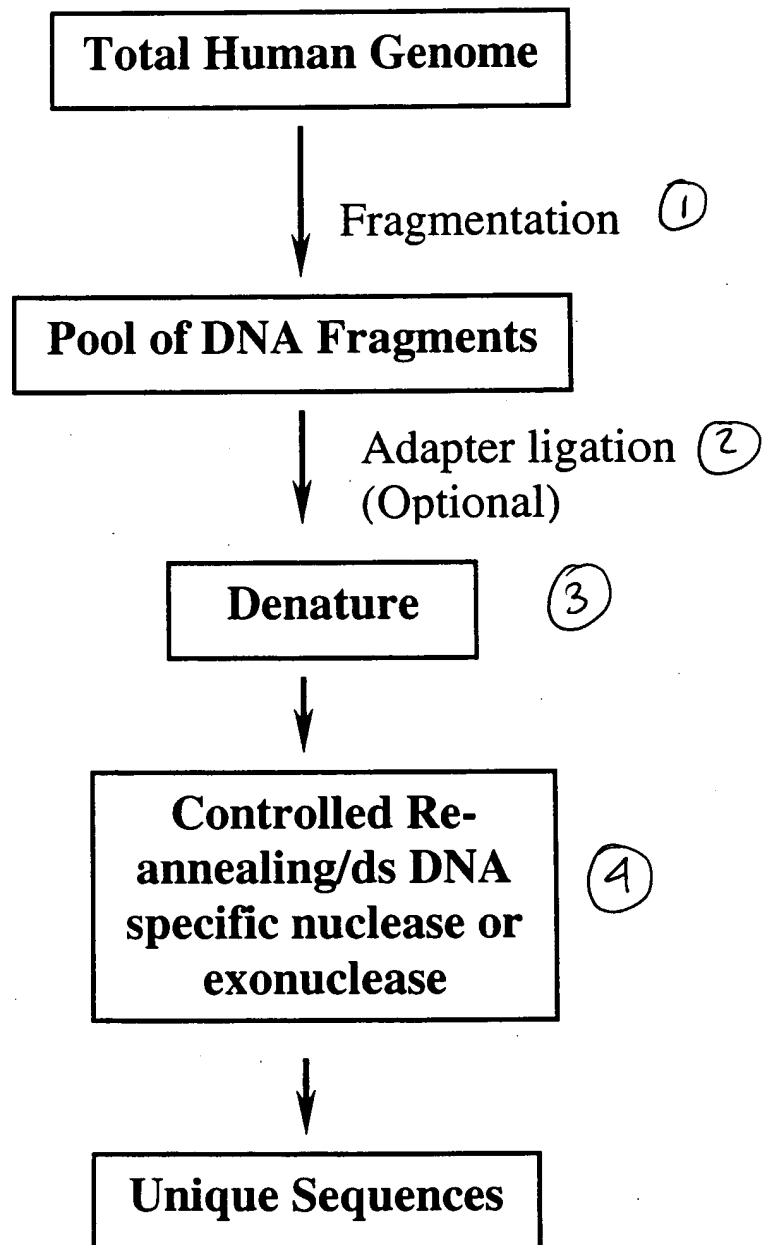


FIGURE 11

Scheme IV

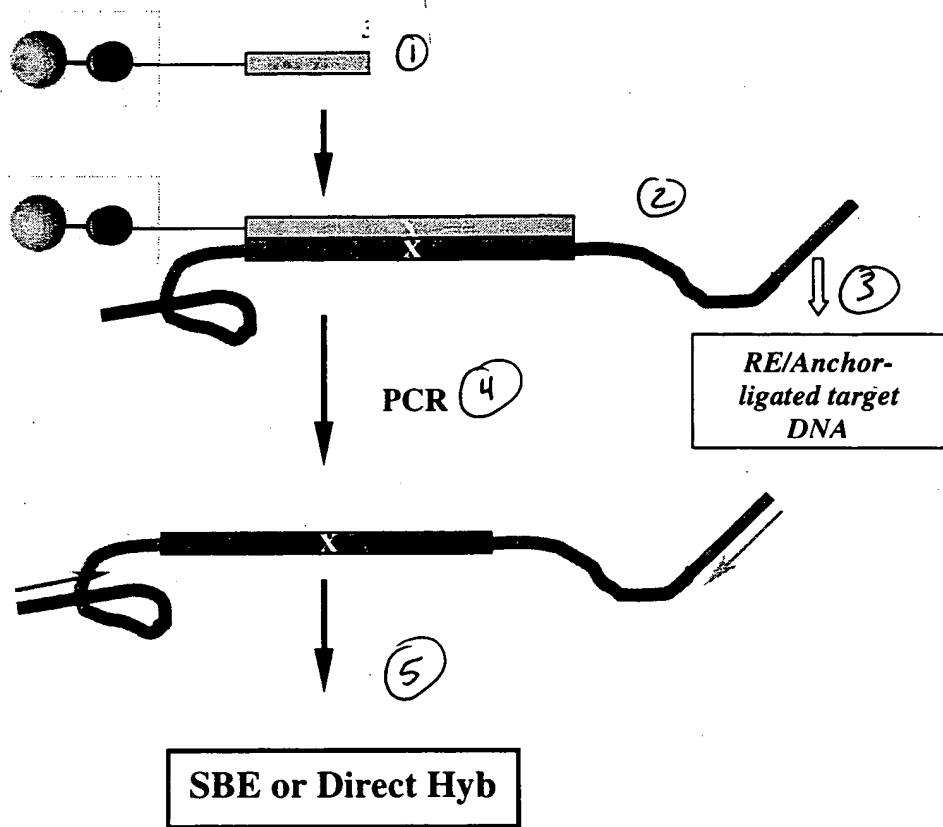


Figure 12

Scheme I

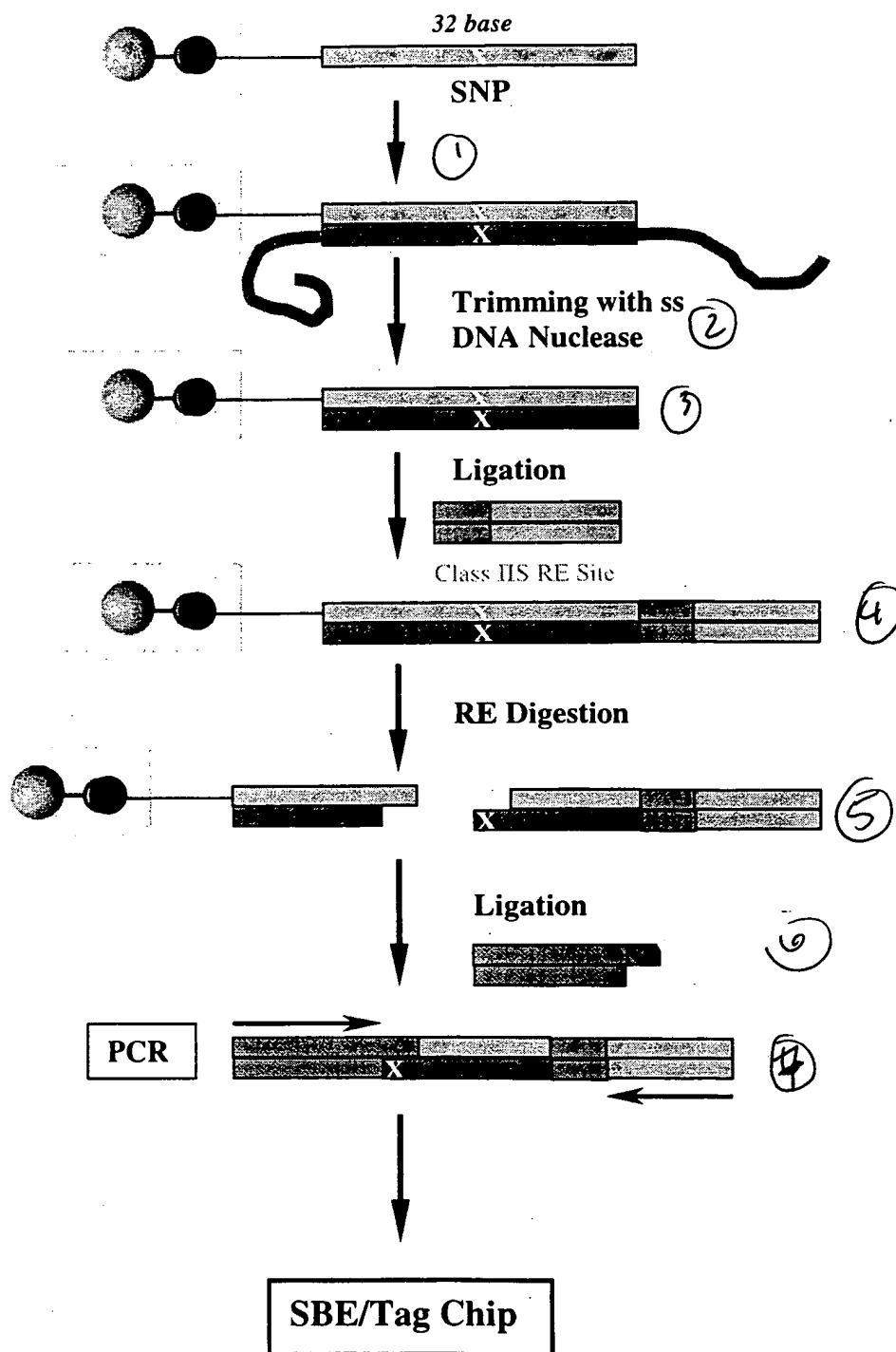


Figure 13

Scheme III

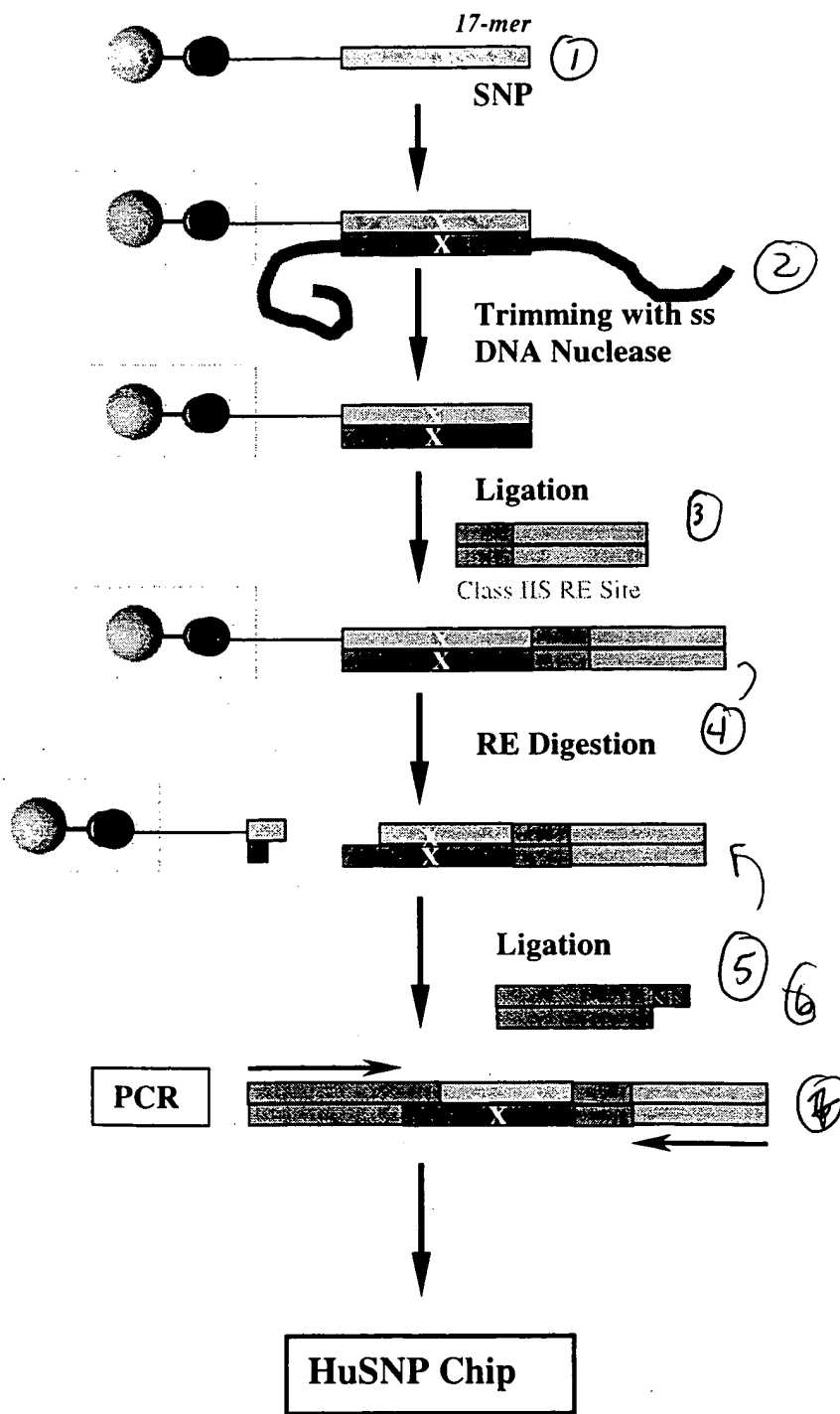


FIGURE 14

Chimeric Probe Array

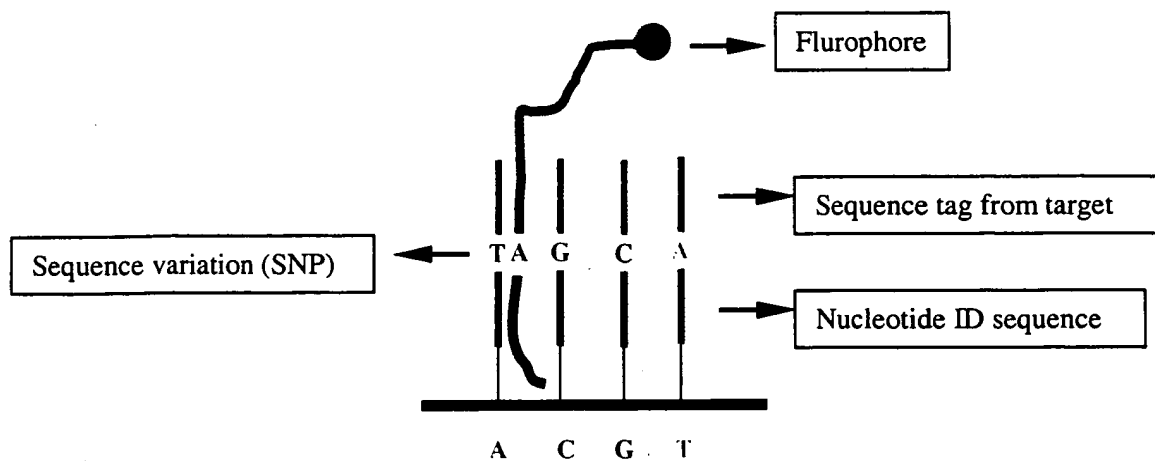


FIGURE 15

Scheme II

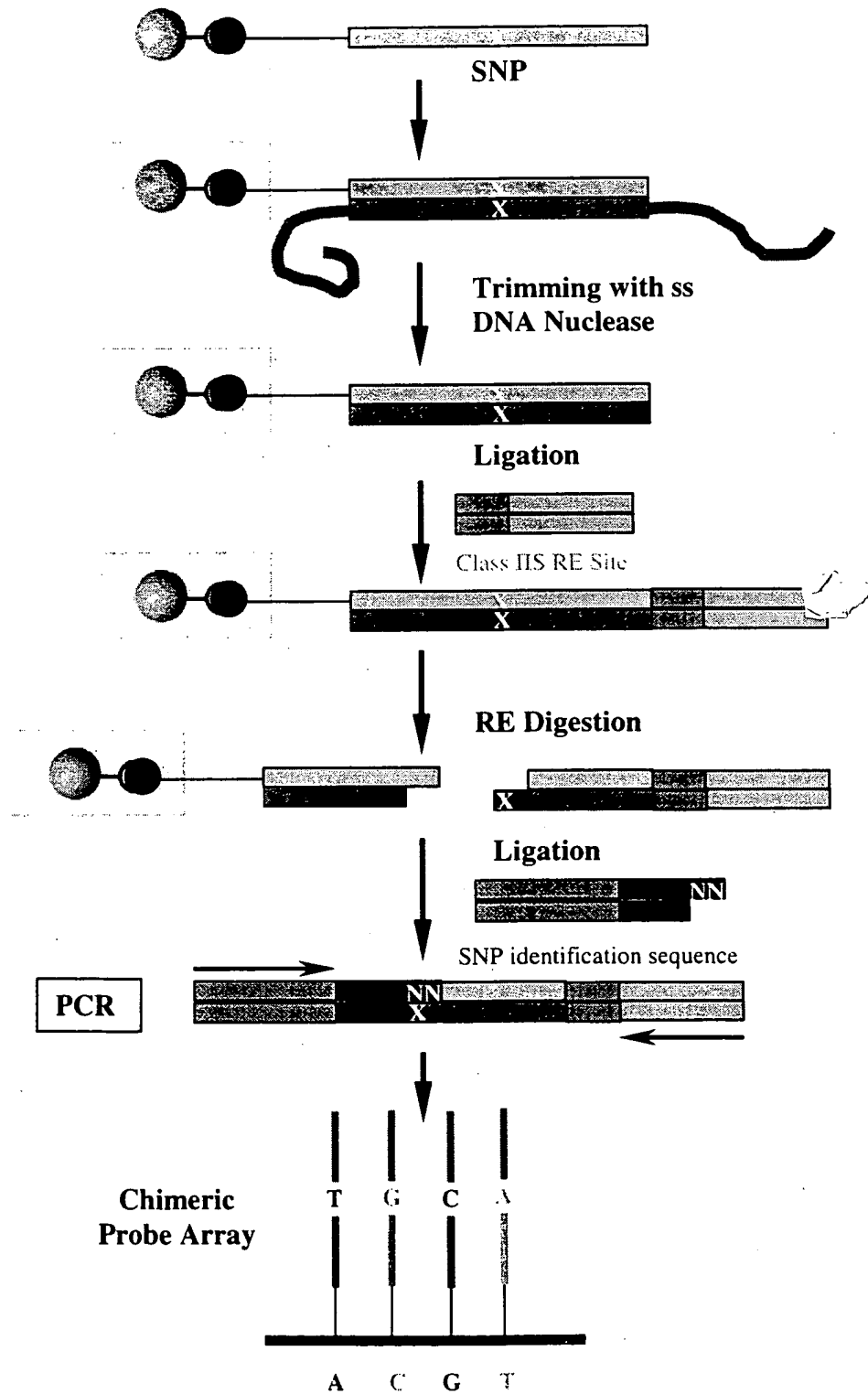


FIGURE 16

## Enrichment of SNPs with MutS Protein

Scheme I

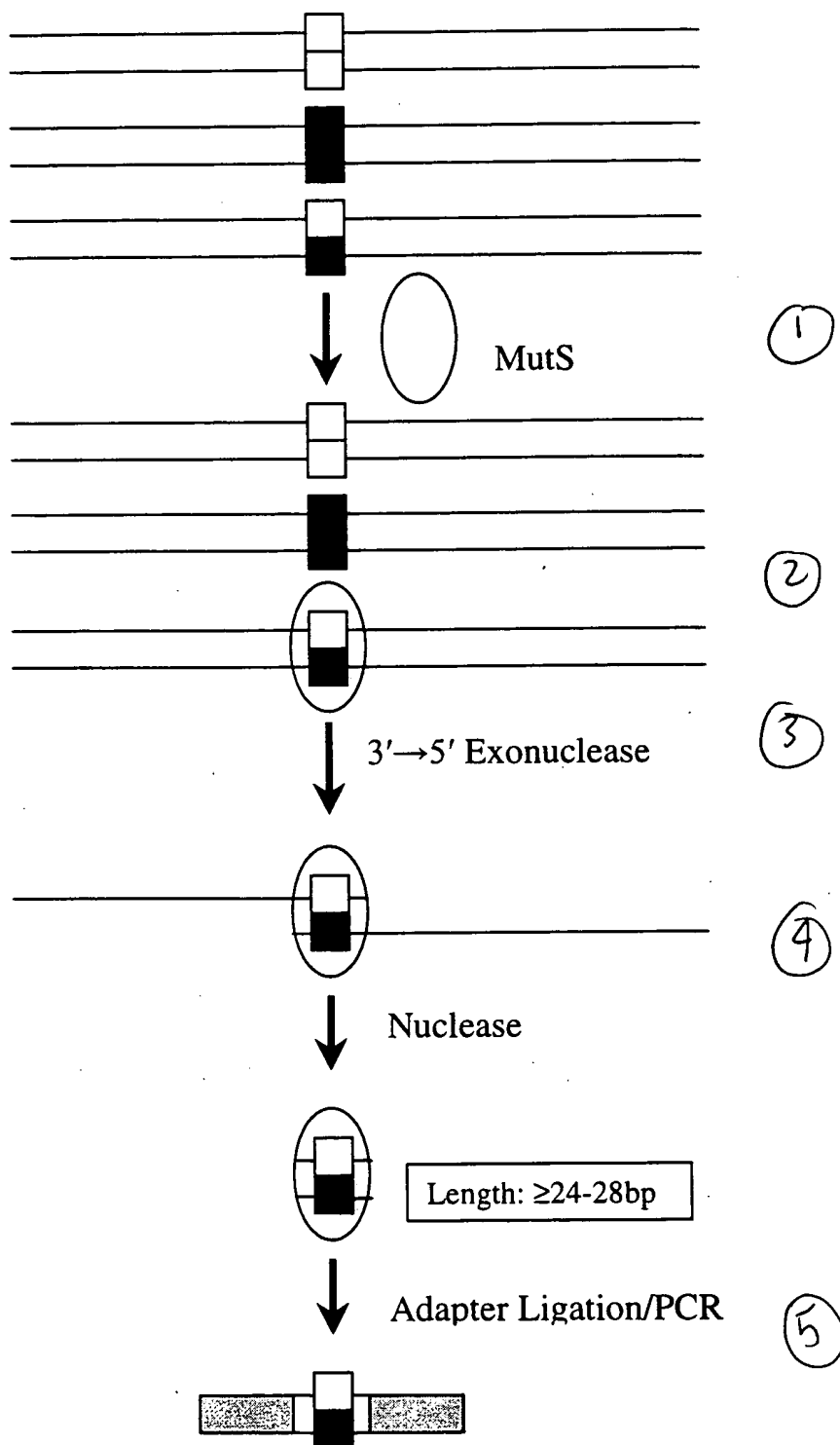
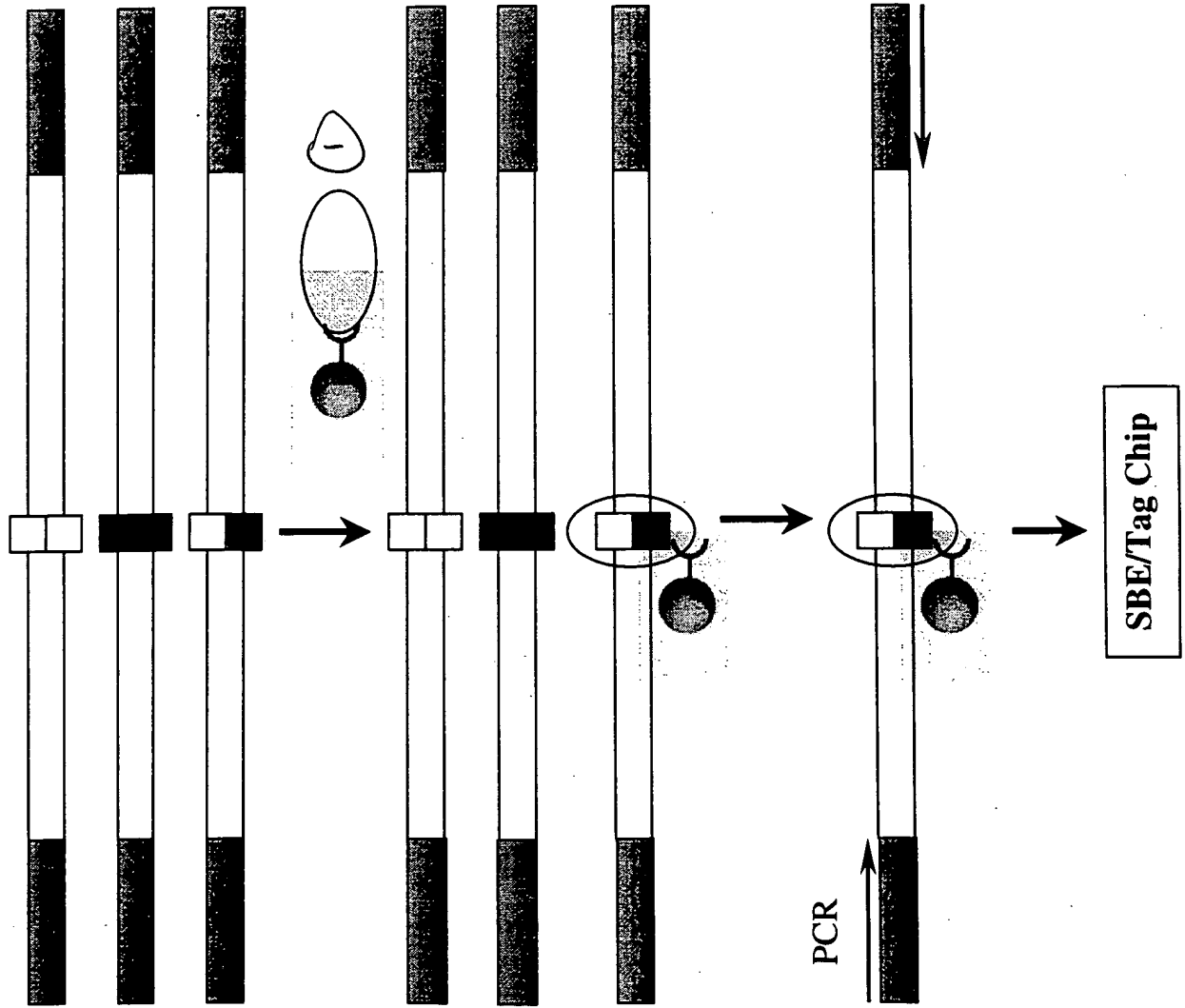




FIGURE 17

Scheme II



Total Genome

+

Rare cutter

Frequent cutter



category I

Frequent

===== Frequent

category II

Rare ===== Rare

category III

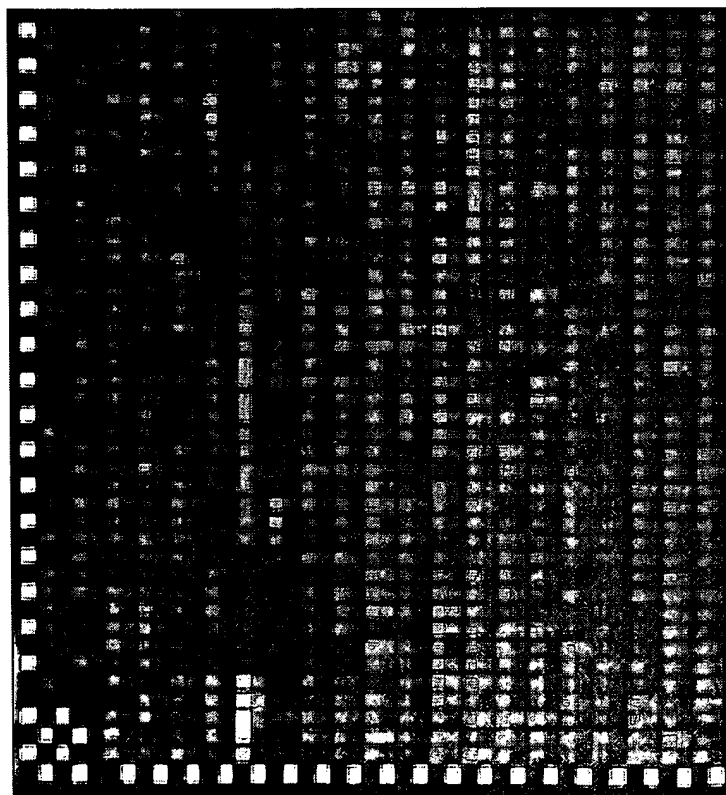
Frequent ===== Rare

Rare ===== Frequent

=====

Figure 19  
Genome

Total Yeast Genome/Y6321D  
10 $\mu$ g/200 $\mu$ l



YGE250-350/Y6321D  
5.24 $\mu$ g/200 $\mu$ l

